

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 04:42:36 ; Search time 70 Seconds
(without alignments)
459.191 Million cell updates/sec

Title: US-09-867-958-1

Perfect score: 849
Sequence: 1 MARQHARTLWYDRPMVFMF.....PPAMDIDDDSDSDADATSN 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPRREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	685	80.7	525	4	Q9BTE6
2	645	76.0	131	11	Q9P9A7
3	642	75.6	140	11	Q9D004
4	340.5	40.1	160	11	Q9D7V0
5	325.5	38.3	241	11	Q9CRH1
6	148	17.4	179	10	Q9FR34
7	131.5	15.5	178	10	Q9FR62
8	125	14.7	371	5	Q9VUX8
9	125	14.7	371	5	Q8STI0
10	122	14.4	190	11	Q09003
11	121	14.3	241	10	Q9FT78
12	121	14.3	262	10	Q81288
13	117	13.8	216	3	Q8X041
14	115	13.5	362	4	Q96T12
15	115	13.5	370	4	Q9N0A7
16	115	13.5	373	4	Q9P035

17	89.5	10.5	305	4	Q9BTE6	Q9BTE6
18	89.5	10.5	484	4	Q13793	Q9BTE6
19	89.5	10.5	547	4	Q13764	Q9BTE6
20	89.5	10.5	695	6	Q9SKN7	Q9BTE6
21	88	10.4	408	10	Q9MAR4	Q9BTE6
22	88	10.4	848	16	Q9TRK7	Q9BTE6
23	84.5	10.0	396	3	Q9USQ4	Q9BTE6
24	84.5	10.0	678	5	Q9V306	Q9BTE6
25	84	9.9	770	6	Q9RUT0	Q9BTE6
26	83.5	9.8	695	11	Q6Q496	Q9BTE6
27	83.5	9.8	695	11	P97487	Q9BTE6
28	82.5	9.7	389	10	Q48706	Q9BTE6
29	82.5	9.7	803	4	Q9P2W4	Q9BTE6
30	82.5	9.7	1226	4	Q9N2B6	Q9BTE6
31	82	9.7	297	10	Q9M4T5	Q9BTE6
32	82	9.7	345	11	Q9JH88	Q9BTE6
33	82	9.7	839	16	Q97F94	Q9BTE6
34	82	9.7	4368	5	Q61851	Q9BTE6
35	81.5	9.6	1430	5	Q23541	Q9BTE6
36	81	9.5	683	5	Q9U3C8	Q9BTE6
37	80	9.4	382	3	Q13782	Q9BTE6
38	80	9.4	512	2	Q43372	Q9BTE6
39	79	9.3	364	11	Q9D1M3	Q9BTE6
40	78.5	9.2	407	5	Q9N6J0	Q9BTE6
41	78.5	9.2	407	5	Q9N6A1	Q9BTE6
42	78.5	9.2	407	5	Q9N613	Q9BTE6
43	78.5	9.2	817	12	Q90761	Q9BTE6
44	78.5	9.2	817	12	Q9J5H1	Q9BTE6
45	77	9.1	593	5	Q97226	Q9BTE6

ALIGNMENTS

RESULT 1

Q9BTE6 PRELIMINARY; PRT: 525 AA.

AC Q9BTE6. 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical 58.8 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE=LUNG;

RC Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC004172; AAH04172.1; -

DR EMBL; BC019324; AAH19324.1; -

DR InterPro; IPR002318; trna-synt_2c.

KW Hypothetical protein

SQ SEQUENCE 525 AA; 58752 MW; 04F376DFD308BC68 CRC64;

Query Match 80.7%; Score 685; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MEFCVEVDSTVHYVLIEDHRIYFSCKNADGVELYNEIEFYAKVNSKDSQDRSSRSITCFV 78
DB 1 MEFCVEVDSTVHYVLIEDHRIYFSCKNADGVELYNEIEFYAKVNSKDSQDRSSRSITCFV 60
QY 79 RKMEKXAMPRLTKEDIKPVWLSYDFDNWRWDEDEMLAHVHYALLKYSIKRPP 138
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Db      61 RRMKEKAMPRLTKEDIKPVWLSVDFDWMRMWEGDEEMELAHVEHYAELLKKVSTKRPP 120
OY      139 AMDDL 144
        |||||
Db      121 AMDDL 126

RESULT 2
OQ9D9A7 PRELIMINARY; PRT; 131 AA.
ID OQ9D9A7;
AC OQ9D9A7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1700113122Rik protein.
GN 1700113122Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK007198; BAB24896.1;
DR MGD: MGI:1920885; 1700113122Rik.
SQ SEQUENCE 131 AA; 15652 MW; 08DD8BAAD081823 CRC64;

Query Match 76.0%; Score 645; DB 11; Length 131;
Best Local Similarity 80.5%; Pred. No. 3.5e-54;
Matches 120; Conservative 4; Mismatches 7; Indels 18; Gaps 1;

OY 1 MARQARTLWDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNNDGVLNIEIFYAKV 60
Db 1 MERQAPRLTWDRPKYVMEFCVEDSTDVSLIEDHRYVFCRNDDGVLNIEIFYAV 60
OY 61 NSKDSQDKRSRSTICFVKKMKKAYAMPRLTKEDIKPVWLSVDFDWMRMWEGDEEMELAH 120
Db 61 NSKDSQDKRSRSTICFVKKMKKAYAMPRLTKEDIKPVWLSVDFDWMRMWEGDEEMELAH 120
OY 121 VEHYAELLKKVSTKRPPAMDDLDDSDS 149
Db 121 VEHYAE-----DDSDS 131

RESULT 3
OQ9D0U4 PRELIMINARY; PRT; 140 AA.
ID OQ9D0U4;
AC OQ9D0U4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1110069E20Rik protein.

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GN 1110069E20Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK004415; BAB23297.1;
DR MGD: MGI:1916146; 1110069E20Rik.
SQ SEQUENCE 140 AA; 16849 MW; 669494AA3F63967 CRC64;

Query Match 75.6%; Score 642; DB 11; Length 140;
Best Local Similarity 88.0%; Pred. No. 7.3e-54;
Matches 117; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY 1 MARQARTLWDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNNDGVLNIEIFYAKV 60
Db 1 MERQAPRLTWDRPKYVMEFCVEDSTDVSLIEDHRYVFCRNDDGVLNIEIFYAV 60
OY 61 NSKDSQDKRSRSTICFVKKMKKAYAMPRLTKEDIKPVWLSVDFDWMRMWEGDEEMELAH 120
Db 61 NSKDSQDKRSRSTICFVKKMKKAYAMPRLTKEDIKPVWLSVDFDWMRMWEGDEEMELAH 120
OY 121 VEHYAELLKKVST 133
Db 121 VEHYAEMHTSHT 133

RESULT 4
OQ9D7V0 PRELIMINARY; PRT; 160 AA.
ID OQ9D7V0;
AC OQ9D7V0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 5730442A20Rik protein.
GN TEBP OR 5730442A20Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

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DR	MGD; MG1:1929282; Tebp.
FT	NON TER
SQ	SEQUENCE 241 AA; 27633 MW; 2E0B776A736985F4 CRC64;
Query Match	
Best Local Similarity 43.8%; Pred. No. 2.5e-23;	
Matches 64; Conservative 24; Mismatches 45; Indels 13; Gaps 2;	
OY	4 OHARTLWDRPMVYMEECVEDSTDVHLLIEDHRIVESC-KNADGVELYNIEFYAKNS 62
	: : : : : : : : : : : : : : :
DB	103 QPSAKMTDRIYVEIEECVEDSKVNANFEKSLTFCGLSDGDNFKHLNEIDLFHCIDP 162
OY	63 KDSODKRSSRSITCFVRKKWEKANPRLTKEIDIKFWMLSVFDNMNRWDGEDEMEALAVE 122
	: : : : : : : : : : : : : : : : :
DB	163 NDSKHRRDRSLTCLCRGSEGSQSMPLRLTEKAKNMILSYFTNNRDMREDDSDDEMSNFE 222
OY	123 HVALIKKYVKTRPPAMDLDSDS 148
	: : : :
DB	223 RESEM-----MDHMGGDED 236
RESULT 6	
O9FR34	PRELIMINARY; PRT; 179 AA.
ID	O9FR34
AC	O9FR34;
DT	01-MAR-2001 (TREMBLrel, 16, Created)
DT	01-MAR-2001 (TREMBLrel, 16, last sequence update)
DT	01-MAR-2001 (TREMBLrel, 16, last annotation update)
DE	Ripening regulated protein DDFR8.
GN	DDFR8.
OS	Lycopersicon esculentum (Tomato).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX	NCBI_TaxID=4081;
RP	[1]
RN	SEQUENCE FROM N.A.
RA	Giovannoni J.J., Yen H., Shelton B., Miller S., Verbalov J.,
RA	Kannan P.,
RT	"Genetic mapping of ripening and ethylene related loci in tomato.";
RL	Theor. Appl. Genet. 98:1005-1013(1999).
DR	EMBL; AF204783; AAC49030.1; "-
SQ	SEQUENCE 179 AA; 20260 MW; C70C3DBBE62B1B0F CRC64;
Query Match	
Best Local Similarity 17.4%; Score 148; DB 10; Length 179,	
Matches 44; Conservative 37; Mismatches 65; Indels 10; Gaps 7;	
OY	4 OHARTLWDRPMVYMEECVEDSTDVHLLIEDHRIVESC-KNADGVELYNIEFYAKVN 61
	: : : : : : : : : : : : : : :
DB	3 RHPTIKWQMSDKLEITVELPDANKWKIKLEBEKFFLESATAGADVNPYEVDLDFKIN 62
OY	62 SKDSODKRSSRSITCFVRKKWEKANPRLTKE-IDIKPYWLTVDPDNMRWDGEDEMETAH 120
	: : : : : : : : : : : : : : : : :
DB	63 VDESSESSTTSIYLVAKAEKD-WMSLVQNGDELGRFLFKVDMDKYVD-EDEDSKNPEP 120
OY	121 VEHVIEL-LKRVSTKRPPAMD---DI DDSDSDAS 151
	: : : : : : : :
DB	121 DMDFGDMDFSKLIMGEGSPNFVDVPECGDDSDTEE 156
RESULT 7	
O9FR62	PRELIMINARY; PRT; 178 AA.
ID	O9FR62
AC	O9FR62;
DT	01-MAR-2001 (TREMBLrel, 16, Created)
DT	01-MAR-2001 (TREMBLrel, 16, last sequence update)
DT	01-MAR-2001 (TREMBLrel, 16, last annotation update)
DE	P23.
GN	P23.
OS	Brassica napus (Rape).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC eurosids II; Brassicales; Brassicaceae; Brassica...
 NX NCBI_TaxID=3708;
 RA [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. TOPAZ;
 RA Cordeneer J.H.G., Jansen H.J., Hause G., Fiers M.A.,
 RA van Lookeren Campagne M.M.;
 RT "np23, the plant ortholog of mammalian p23, is upregulated during
 RT microspore embryogenesis in Brassica napus";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF153128; AAC41763.1;
 SO SEQUENCE 178 AA; 20096 MW; 216E6DA677FE46A CRC64;
 QY Query Match 15.5%; Score 131.5; DB 10; Length 178;
 Best Local Similarity 32.2%; Pred. No. 6; Le-05;
 Matches 37; Conservative 25; Mismatches 48; Indels 5; Gaps 5;
 Db 3 RHPIVKNRQSDWYIYELPDADVDKLEPEGKFFSATSASGASKTILEVDLDDSDV 62
 QY 62 SKSDSRKSSRSITCFVKKMKKXVAMPRLTKEDIK-PWLVSDPDMRDWEGDEE 115
 Db 63 VNEKASVSSNSVYLVKKAESK-WNRRLTKPEGKHPIYLVKMDKWD-EDDED 115
 RESULT 8
 Q9VJX8 PRELIMINARY; PRT; 371 AA.
 AC Q9VJX8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE CG9267 protein.
 GN CG9267.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sulten G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cateley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertlera S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison D.R., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003640; AAF53307.1;
 DR FLYBASE: FBgn0032524; CG9267.
 SO SEQUENCE 371 AA; 43682 MW; C23D7394BDFC2968 CRC64;
 QY Query Match 14.7%; Score 125; DB 5; Length 371;
 Best Local Similarity 36.2%; Pred. No. 0.00062;
 Matches 34; Conservative 13; Mismatches 37; Indels 10; Gaps 4;
 Db 47 ARGVAVYFELHFTALIDENATFVSDNKIELOIRK-LEPEWMPRLVATPQPHMLKID 105
 QY 104 FDMWRDMEGDEME-----LAHVEHYAELLKK 130
 Db 106 FDMWRFT-EDDVEVEKPRDVRDYEKEYADLOKR 138
 RESULT 9
 Q8SYT0 PRELIMINARY; PRT; 371 AA.
 AC Q8SYT0;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RE57556P.
 GN CG9267.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brockstein P., Hong L., Aghayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY071533; AAL49155.1;
 SO SEQUENCE 371 AA; 43622 MW; C228939B5DE62968 CRC64;
 QY Query Match 14.7%; Score 125; DB 5; Length 371;
 Best Local Similarity 36.2%; Pred. No. 0.00062;
 Matches 34; Conservative 13; Mismatches 37; Indels 10; Gaps 4;
 Db 45 ADGVELYN-EIEFYAKVSKDSQSRSSITCFVKKMKKXVAMPRLTKEDIKPWLVSD 103
 QY 47 ARGVAVYFELHFTALIDENATFVSDNKIELOIRK-LEPEWMPRLVATPQPHMLKID 105
 Db 104 FDMWRDMEGDEME-----LAHVEHYAELLKK 130
 Db 106 FDMWRFT-EDDVEVEKPRDVRDYEKEYADLOKR 138
 RESULT 10
 Q09003 PRELIMINARY; PRT; 190 AA.
 AC Q09003;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE B-IND1 protein (Fragment).
 GN HSPC121 OR B-IND1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RX NCBI_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20286798; PubMed=10747961;
 RA Courilleau D., Chastre E., Sabbah M., Redeuilh G., Afifi A., Meister J.,
 RT "B-Ind1, a novel mediator of Rac1 signalling cloned from sodium
 RT butyrate-treated fibroblasts."
 RL J. Biol. Chem. 275:17344-17348(2000).
 DR EMBL: 297207; CAB10097.2;
 FT MGD; MGI:1869341; Hspc121.
 FT NON_TER
 SQ SEQUENCE 190 AA; 22674 MW; 6499729FC2FA549 CRC64;

Query Match 14.4%; Score 122; DB 11; Length 190;
 Best Local Similarity 30.2%; Pred. No. 0.00053;
 Matches 39; Conservative 25; Mismatches 57; Indels 8; Gaps 6;

OY 10 WYDRPMVFMFCVEDSTDVHLIEDHRIYVSC--NADGVELYN-EIEFYAKNSKDSQ 66
 DB 12 WAQRHRLYRVELSDYQNPALSTIDVLFKAGHGKGNVTEFLFEDLVKPEPAY 71
 OY 67 DKRSSITCFVRKWKKEKVAWPRLTKEIKPVLSDVDNWRDWDGDEMEMLAHEHYAE 126
 DB 72 -RLTGROVNTVYOK-KGSHWMERLTKEKRPFLAPDFDRWLD-ESDAEMLRKKEE--E 126
 OY 127 LKKVSTKR 135
 DB 127 RLRKRLER 135

RESULT 11
 O9FT78 PRELIMINARY; PRT; 241 AA.
 AC 09FT78;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE P23 co-chaperone.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 RX NCBI_TaxID=3702;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Bowra S.;
 RT "A plant p23: the missing link suggesting glucocorticoid receptors
 RT exist in plants."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1297951; CAC16575.1;
 SQ SEQUENCE 241 AA; 25455 MW; 90989FE9550BDC3D CRC64;

Query Match 14.3%; Score 121; DB 10; Length 241;
 Best Local Similarity 27.6%; Pred. No. 0.00088;
 Matches 35; Conservative 25; Mismatches 57; Indels 10; Gaps 5;

OY 4 QHARTLWDRPMVFMFCVEDSTDVHLIEDHRIY-FSCKNADGVELYN-EIEFYAKVN 61
 DB 3 RHPEVKWAETTERKIFLVVLADTKDTKYNLDPEGVFDSAKVGEPENHYELKLELADKVN 62
 OY 62 SKDSQDKRSSRSTCFVRKWKKEKVAWPRLTKEIKPVLSDVDNWRDWDGDE-----E 115
 DB 63 VEESKINIGERSIFCIIEK-AEPERWKMLLRKRPYKVKVDMKWDV-EDDEGSAGAAD 120
 OY 116 MELAHVE 122
 DB 121 MDMAAME 127

RESULT 12
 ID 081288 PRELIMINARY; PRT; 262 AA.
 AC 081288;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE T14P8.5 protein.
 GN T14P8.5 OR A74G02450.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 RX NCBI_TaxID=3702;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. COLUMBIA;
 RA WASHU;
 RT "The A. thaliana Genome Sequencing Project."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Kalicki J., Elliott G., Cloud J.;
 RT "The sequence of A. thaliana T14P8."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 13
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN 14
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN 15
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF069298; AAC19287.1;
 DR EMBL: AL161494; CAB80738.1;
 KW Hypothetical protein.
 SQ SEQUENCE 262 AA; 27944 MW; 67BBF89EEF6625D6 CRC64;

Query Match 14.3%; Score 121; DB 10; Length 262;
 Best Local Similarity 27.6%; Pred. No. 0.00098;
 Matches 35; Conservative 25; Mismatches 57; Indels 10; Gaps 5;

OY 4 QHARTLWDRPMVFMFCVEDSTDVHLIEDHRIY-FSCKNADGVELYN-EIEFYAKVN 61
 DB 7 RHPEVKWAETTERKIFLVVLADTKDTKYNLDPEGVFDSAKVGEPENHYELKLELADKVN 66
 OY 62 SKDSQDKRSSRSTCFVRKWKKEKVAWPRLTKEIKPVLSDVDNWRDWDGDE-----E 115
 DB 67 VEESKINIGERSIFCIIEK-AEPERWKMLLRKRPYKVKVDMKWDV-EDDEGSAGAAD 124
 OY 116 MELAHVE 122
 DB 125 MDMAAME 131

RESULT 13
 ID 08X041 PRELIMINARY; PRT; 216 AA.
 AC 08X041;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Related to Hsp90 associated co-chaperone.
 GN BIK1.180.
 OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nykatura G., Mewes H.W., Manhaupt G.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL669998; CAD21185.1; -
 SQ SEQUENCE 216 AA; 23599 MW; 861F66CF350A61BF CRC64;

Query Match 13.8%; Score 117; DB 3; Length 216;
 Best Local Similarity 32.1%; Pred. No. 0.0019;
 Matches 35; Conservative 26; Mismatches 40; Indels 8; Gaps 5;

QY 16 YFMECEVD--STDVHVLIEDHRIYFSCKNADGVLYN-EIEFYAKVNSKDSQDKRSSR 72
 Db 24 FYLTISVPDVPSTNLKLDLKPGLTGHSDTLKRTYHVEFYAEIDPAAQVHHTAR 83
 QY 73 SITCFYRKKEKYA--WPRLTKEIDIPVWLSYDFDNMRDMEGDEMEELAE 119
 Db 84 DYEMLRK-KEIDAHYPRLLKPKVHFLKTDFFDKWD--EDEQHFAA 129

RESULT 14

096712 PRELIMINARY; PRT; 362 AA.

AC 096712:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE CDNA FLJ14515 fis, clone NRZRM1000800, weakly similar to Mus
 DE musculus partial B-IND1 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murekami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
 RA Ninomiya K., Iwayanagi T.,
 RT "NEO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027421; BAB55101.1; -
 SQ SEQUENCE 362 AA; 43158 MW; EB371D668DDCF075 CRC64;

Query Match 13.5%; Score 115; DB 4; Length 362;
 Best Local Similarity 29.6%; Pred. No. 0.0054;
 Matches 37; Conservative 24; Mismatches 56; Indels 8; Gaps 5;

QY 10 WYDRPMYFMECEVDSTDVHVLIEDHRIYFSCKNADGVLYN-EIEFYAKVNSKDSQ 66
 Db 12 WQHRHRELTLRELSDVQNPALSTENVLHFKAG-CHGAKGDVYEFHLFLDLVKKPEPV 70
 QY 67 DKRSSRSTCFYRKKEKYAWPRLTKEIDIPVWLSYDFDNMRDMEGDEMEELAEVHYAE 126
 Db 71 YKLTQGVNITVOK-KVSQWMERLTQEKRRPLFLAPDFDRWD-ESDAEMELRAKEE--E 126
 QY 127 LKKV 131
 Db 127 LKKV 131

RESULT 15

09NOA7
 ID 09NOA7 PRELIMINARY; PRT; 370 AA.

AC 09NOA7:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE B-ind1 protein.
 GN B-IND1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20298798; PubMed=10747961;
 RA Courtilleau D., Chastre E., Sabbah M., Redeuilh G., Affi A., Mester J.,
 RT "B-ind1, a novel mediator of Rac1 signalling cloned from sodium
 butyrate-treated fibroblasts."
 RL J. Biol. Chem. 275:17344-17348(2000).
 DR EMBL: AJ2771091; CAB69070.1; -
 SQ SEQUENCE 370 AA; 43543 MW; 2D1E8ED1658BF00 CRC64;

Query Match 13.5%; Score 115; DB 4; Length 370;
 Best Local Similarity 30.4%; Pred. No. 0.0056;
 Matches 38; Conservative 23; Mismatches 56; Indels 8; Gaps 6;

QY 10 WYDRPMYFMECEVDSTDVHVLIEDHRIYFSC--NADGVLYN-EIEFYAKVNSKDSQ 66
 Db 12 WQHRHRELTLRELSDVQNPALSTENVLHFKAGHAGKGDVYEFHLFLDLVKKPEPV 71
 QY 67 DKRSSRSTCFYRKKEKYAWPRLTKEIDIPVWLSYDFDNMRDMEGDEMEELAEVHYAE 126
 Db 72 -KLTQGVNITVOK-KVSQWMERLTQEKRRPLFLAPDFDRWD-ESDAEMELRAKEE--E 126
 QY 127 LKKV 131
 Db 127 LKKV 131

Search completed: March 20, 2003, 05:20:07
 Job time : 80 secs